

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 3, 2005, 23:17:42 ; Search time 101 Seconds

(without alignments)  
3127.531 Million cell updates/sec

Title: US-10-071-838-2  
Perfect score: 2983  
Sequence: 1 MDVAVGASWMAQEREDILM.....TSGECLGHLHSSQFPPEGF 549

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2983	100.0	549	1 TBC3_HUMAN	Q81ZPI1 homo sapien
2	2971	99.6	549	2 O6IPX1	Q61PZ1 homo sapien
3	2971	99.6	549	2 AAH71680	AAH71680 homo sapi
4	2945	98.7	549	2 O6DH75	Q6DH75 homo sapien
5	2188.5	73.4	1406	1 DBP6_HUMAN	P35123 homo sapien
6	1544.5	51.8	376	2 O15635	Q15635 homo sapien
7	1479	49.6	346	2 O6PD72	Q6PD72 homo sapien
8	1479	49.6	346	2 AAH58890	AAH58890 homo sapi
9	1477.5	49.5	376	2 O6PI12	Q6PI12 homo sapien
10	1477.5	49.5	376	2 AAH33670	AAH33670 homo sapi
11	1346	45.1	291	2 O6DCB4	Q6DCB4 homo sapien
12	655	22.0	819	1 US6L_MOUSE	Q80XC3 mus musculu
13	655	22.0	841	1 BAC97847	BAC97847 mus muscu
14	651	21.8	828	1 US6L_HUMAN	Q92738 homo sapien
15	651	21.8	838	2 BAA02807	BAA02807 homo sapi
16	603.5	20.2	250	2 O6BND7	Q6BND7 homo sapien
17	602	20.2	224	2 O8NC5	Q8NC5 homo sapien
18	576	19.3	1085	2 O9U2D8	Q9U2D8 caenorhabdi
19	576	19.3	1085	2 CAB60374	CAB60374 caenorhab
20	574.5	19.3	1021	2 O7K711	O7K711 caenorhabdi
21	574.5	19.3	1021	2 CAB45741	CAB45741 caenorhab
22	530	17.8	391	2 O7QFV5	Q7QFV5 anopheles g
23	500.5	16.8	498	2 O7PPV8	Q7PPV8 anopheles g
24	455	15.3	457	2 O18357	O18357 dirosophila
25	455	15.3	485	2 O95R80	O95R80 dirosophila
26	455	15.3	571	2 O7KR75	O7KR75 dirosophila
27	323.5	10.8	356	2 O81347	O81347 arabidopsis
28	321.5	10.8	537	2 O8BHJ3	O8BHJ3 mus musculu
29	321.5	10.8	537	2 O91XR3	O91XR3 mus musculu
30	321.5	10.8	655	2 O6GQW9	O6GQW9 mus musculu
31	320.5	10.7	533	2 Q9H822	Q9H822 homo sapien

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32	320.5	10.7	584	2 O6IN54	Q6IN54 homo sapien
33	320.5	10.7	584	2 AAH72453	AAH72453 homo sapi
34	320.5	10.7	622	2 O6P530	O6P530 homo sapien
35	320.5	10.7	622	2 AAH63112	AAH63112 homo sapi
36	319	10.7	353	2 O8LAF3	O8LAF3 arabidopsis
37	317.5	10.6	304	2 O9M894	O9M894 arabidopsis
38	306.5	10.3	532	2 O9Y1V8	O9Y1V8 halocynthia
39	305.5	10.2	500	1 TB10_MOUSE	P58802 mus musculu
40	302	10.1	298	2 O81V04	O81V04 mus musculu
41	301	10.1	446	2 O81V04	O81V04 mus musculu
42	301	10.1	446	2 AAH62999	AAH62999 homo sapi
43	301	10.1	450	2 AAH36873	AAH36873 homo sapi
44	300	10.1	500	2 O8C162	O8C162 mus musculu
45	299.5	10.0	508	1 TB10_HUMAN	Q9BX16 homo sapien

## ALIGNMENTS

RESULT 1  
ID TBC3\_HUMAN STANDARD; PRT; 549 AA.  
AC O81ZPI, O9H0B9; Q9UDD4;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE TBC1 domain family member 3 (Rab GTPase-activating protein PRCI7)  
DE (Prostate cancer gene 17 protein) (TREI7 alpha protein).  
GN Name=TBC1D3; Synonyms=PRCI7;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=22246263; PubMed=12359748;  
RX Pei L., Peng Y., Yang Y., Ling X.B., Van Eyndhoven W.G., Nguyen K.C.,  
RA Rubin M., Hoey T., Powers S., Li J.,  
RT "PRCI7", a novel oncogene encoding a Rab GTPase-activating protein, is  
RT amplified in prostate cancer.";  
RL Cancer Res. 62:5420-5424(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Testis;  
RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;  
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glaesl S.,  
RA Amorge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,  
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,  
RA Mewes H.-W., Osternwalder B., Obermaier B., Jampé U., Heubner D.,  
RA Wandt R., Korn B., Klein W., Poustka A.,  
RT "Towards a catalog of human genes and proteins: sequencing and  
RT analysis of 500 novel complete protein coding human cDNAs.";  
RL Genome Res. 11:422-435(2001).  
RN [3]  
RP SEQUENCE OF 1-52 FROM N.A.  
RX MEDLINE=93228825; PubMed=8471161;  
RA Ono M., Nakamura T., Mariga-Samson R., Hillova J., Hill M.,  
RT "Human TREI7 oncogene is generated from a family of homologous  
RT polymorphic sequences by single-base changes.";  
RL DNA Cell Biol. 12:107-118(1993).  
RN [4]  
RP SEQUENCE OF 1-52 FROM N.A.  
RX TISSUE=Placenta;  
RX MEDLINE=94010310; PubMed=8406013;  
RA Ono M., Nakamura T., Hillova J., Hill M.,  
RT "Identification of novel sequences in the repertoire of hypervariable  
RT TREI7 genes from immortalized normal and malignant human  
RT keratinocytes.";  
RL Gene 131:209-215(1993).  
RN [5]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=22506395; PubMed=12604796; DOI=10.1073/pnas.0437015100;  
RA Paulding C.A., Ruvoio M., Haber D.A.;

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RT "The Tre2 (USP6) oncogene is a hominoid-specific gene."  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:2507-2511(2003).  
 CC -1- FUNCTION: Acts as a GTPase activating protein for RAB5. Does not  
 CC act on RAB4 or RAB11.  
 CC -1- TISSUE SPECIFICITY: Expressed in liver, skeletal muscle, kidney,  
 CC pancreas, spleen, testis, ovary, small intestine and peripheral  
 CC blood leukocytes. Overexpressed in prostate cancers.  
 CC -1- DISEASE: May be involved in forms of prostate cancers.  
 CC -1- SIMILARITY: Contains 1 Rab-GAP TBC domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: AF540953; MAN3117.1; -  
 DR EMBL: ALJ36860; CAB6794.1; -  
 DR EMBL: X71377; CAB94197.1; -  
 DR Genew: HGNC:19031; TBC1D3.  
 DR MIM: 607741; -  
 DR InterPro: IPR000195; RabGAP\_TBC.  
 DR Pfam: PF00566; TBC; 1.  
 DR SMART: SM00164; TBC; 1.  
 DR PROSITE: PS50086; TBC\_RABGAP; 1.  
 DR GTPase activation; Proto-oncogene.  
 KW DOMAIN 101 293 Rab-GAP TBC.  
 FT CONFLICT 117 177 I -> T (in Ref. 2).  
 FT CONFLICT 137 137 R -> K (in Ref. 2).  
 FT CONFLICT 354 354 Q -> K (in Ref. 2).  
 FT CONFLICT 526 526 P -> Q (in Ref. 2).  
 SQ SEQUENCE 549 AA; 62168 MW; 831DA747D0B6F400 CRC64;  
 Query Match 100.0%; Score 2983; DB 1; Length 549;  
 Best Local Similarity 100.0%; Pred. No. 1,4e-179; Indels 0; Gaps 0;  
 Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MDVVEVAGSWMAOEREDIIIMKYEKGHRAGLPEDKGPFRSYNNVNDHGIYHETELPPL 60  
 DB 1 MDVVEVAGSWMAOEREDIIIMKYEKGHRAGLPEDKGPFRSYNNVNDHGIYHETELPPL 60  
 QY 61 TABBAKQIRREISRSKSWVDMLGDMWEKYSRKLIDRAYKGMNIRGPMWSVLTINTEEM 120  
 DB 61 TABBAKQIRREISRSKSWVDMLGDMWEKYSRKLIDRAYKGMNIRGPMWSVLTINTEEM 120  
 QY 121 KLNKPGRYQIMKEKGRSSSEHIQRIIDRVSGTLRKHIFFRDRYGTQKORELHILLAYEEX 180  
 DB 121 KLNKPGRYQIMKEKGRSSSEHIQRIIDRVSGTLRKHIFFRDRYGTQKORELHILLAYEEX 180  
 QY 181 NPEVGYCRDLISHIALFLYLTPBEDAFWALVOLLASERHSLOGFHSFNGSTVOGLDQOE 240  
 DB 181 NPEVGYCRDLISHIALFLYLTPBEDAFWALVOLLASERHSLOGFHSFNGSTVOGLDQOE 240  
 QY 241 HVAATQPKTMGQDKDLGCGQSPGLCLRLILIDGSLGLTLRLMDVYLVEGSOALMPI 300  
 DB 241 HVAATQPKTMGQDKDLGCGQSPGLCLRLILIDGSLGLTLRLMDVYLVEGSOALMPI 300  
 QY 301 TRIAFKVOQRLTKTSRCGPMARFCRFVDTMAEDBTPLVLAHLSKMKLTRKQGLDPPP 360  
 DB 301 TRIAFKVOQRLTKTSRCGPMARFCRFVDTMAEDBTPLVLAHLSKMKLTRKQGLDPPP 360  
 QY 361 AKEDQSSASRPVPSASRGKTLCKGRDQAPPGPARPPRPRIWASPPRARSSSTPCGGA 420  
 DB 361 AKEDQSSASRPVPSASRGKTLCKGRDQAPPGPARPPRPRIWASPPRARSSSTPCGGA 420  
 QY 421 VREDTTPVGTQGPSPLAAGGPGGSRFPLOMNSMPLPTDLVDGEGFPHYDFRQSCWV 480  
 DB 421 VREDTTPVGTQGPSPLAAGGPGGSRFPLOMNSMPLPTDLVDGEGFPHYDFRQSCWV 480  
 QY 481 RAISOEDQLAPCWAHEPARVRSAPAPSTDSOGTFRARDEOPCAPTSGPLCGLHL 540

DB 481 RAISOEDQLAPCWAHEPARVRSAPAPSTDSOGTFRARDEOPCAPTSGPLCGLHL 540  
 QY 541 ESSQFPFPGF 549  
 DB 541 ESSQFPFPGF 549  
 RESULT 2  
 ID 06IPX1 PRELIMINARY; PRT; 549 AA.  
 AC 06IPX1;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE TBC1 domain family, member 3.  
 GN Name=TBC1D3;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,  
 RA Diatchenko L., Matsushita K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.U., Usdin T.B., Toshiyuki S., Carninci P., Piatte C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
 RA Krzywicki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC071680; AAH71680.1; -  
 DR InterPro: IPR000195; RabGAP\_TBC.  
 DR Pfam: PF00566; TBC; 1.  
 DR SMART: SM00164; TBC; 1.  
 DR PROSITE: PS50086; TBC\_RABGAP; 1.  
 SQ SEQUENCE 549 AA; 62231 MW; 5657E5602B3655F5 CRC64;  
 Query Match 99.6%; Score 2971; DB 2; Length 549;  
 Best Local Similarity 99.5%; Pred. No. 8.2e-179;  
 Matches 546; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MDVVEVAGSWMAOEREDIIIMKYEKGHRAGLPEDKGPFRSYNNVNDHGIYHETELPPL 60  
 DB 1 MDVVEVAGSWMAOEREDIIIMKYEKGHRAGLPEDKGPFRSYNNVNDHGIYHETELPPL 60  
 QY 61 TABBAKQIRREISRSKSWVDMLGDMWEKYSRKLIDRAYKGMNIRGPMWSVLTINTEEM 120  
 DB 61 TABBAKQIRREISRSKSWVDMLGDMWEKYSRKLIDRAYKGMNIRGPMWSVLTINTEEM 120  
 QY 121 KLNKPGRYQIMKEKGRSSSEHIQRIIDRVSGTLRKHIFFRDRYGTQKORELHILLAYEEX 180  
 DB 121 KLNKPGRYQIMKEKGRSSSEHIQRIIDRVSGTLRKHIFFRDRYGTQKORELHILLAYEEX 180  
 QY 181 NPEVGYCRDLISHIALFLYLTPBEDAFWALVOLLASERHSLOGFHSFNGSTVOGLDQOE 240  
 DB 181 NPEVGYCRDLISHIALFLYLTPBEDAFWALVOLLASERHSLOGFHSFNGSTVOGLDQOE 240